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RAW SEQUENCE LISTING

DATE: 09/25/2001

PATENT APPLICATION: US/09/919,408

TIME: 09:56:50

Input Set : N:\Crf3\RULE60\09919408.txt

Output Set: N:\CRF3\09252001\I919408.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: Lemischka, Ihor R.

8 (ii) TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
9 RECEPTORS AND THEIR LIGANDS

11 (iii) NUMBER OF SEQUENCES: 10

13 (iv) CORRESPONDENCE ADDRESS:

14 (A) ADDRESSEE: ImClone Systems Incorporated

15 (B) STREET: 180 Varick Street

16 (C) CITY: New York

17 (D) STATE: New York

18 (E) COUNTRY: U.S.A.

19 (F) ZIP: 10014

21 (v) COMPUTER READABLE FORM:

22 (A) MEDIUM TYPE: Floppy disk

23 (B) COMPUTER: IBM PC compatible

24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

27 (vi) CURRENT APPLICATION DATA:

C--> 28 (A) APPLICATION NUMBER: US/09/919,408

C--> 29 (B) FILING DATE: 31-Jul-2001

30 (C) CLASSIFICATION:

64 (vii) PRIOR APPLICATION DATA:

33 (A) APPLICATION NUMBER: 07/977,451

34 (B) FILING DATE:

37 (A) APPLICATION NUMBER: US 07/906,397

38 (B) FILING DATE: 26-JUN-1992

41 (A) APPLICATION NUMBER: US PCT/US92/05401

42 (B) FILING DATE: 26-JUN-1992

45 (A) APPLICATION NUMBER: TW 81102961

46 (B) FILING DATE: 15-APR-1992

49 (A) APPLICATION NUMBER: US PCT/US92/02750

50 (B) FILING DATE: 02-APR-1992

53 (A) APPLICATION NUMBER: US 07/813,593

54 (B) FILING DATE: 24-DEC-1991

57 (A) APPLICATION NUMBER: US 07/793,065

58 (B) FILING DATE: 15-NOV-1991

61 (A) APPLICATION NUMBER: US 07/728,913

62 (B) FILING DATE: 28-JUN-1991

65 (A) APPLICATION NUMBER: US 07/679,666

66 (B) FILING DATE: 02-APR-1991

68 (viii) ATTORNEY/AGENT INFORMATION:

69 (A) NAME: Feit, Irving N.

70 (B) REGISTRATION NUMBER: 28,601

71 (C) REFERENCE/DOCKET NUMBER: LEM-3-7P

73 (ix) TELECOMMUNICATION INFORMATION:

74 (A) TELEPHONE: 212-645-1405

ENTERED

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75          (B) TELEFAX: 212-645-2054
78 (2) INFORMATION FOR SEQ ID NO: 1:
80      (i) SEQUENCE CHARACTERISTICS:
81          (A) LENGTH: 3453 base pairs
82          (B) TYPE: nucleic acid
83          (C) STRANDEDNESS: double
84          (D) TOPOLOGY: linear
86      (ii) MOLECULE TYPE: cDNA
88      (iii) HYPOTHETICAL: NO
90      (iv) ANTI-SENSE: NO
92      (v) FRAGMENT TYPE: N-terminal
95      (ix) FEATURE:
96          (A) NAME/KEY: mat_peptide
97          (B) LOCATION: 112..3006
99      (ix) FEATURE:
100         (A) NAME/KEY: sig_peptide
101         (B) LOCATION: 31..111
103      (ix) FEATURE:
104         (A) NAME/KEY: CDS
105         (B) LOCATION: 31..3009
108      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
110 GCGGCCTGCG TACCGCGCGC TCCGGAGGCC ATG CGG GCG TTG GCG CAG CGC AGC      54
111                               Met Arg Ala Leu Ala Gln Arg Ser
112                               -27   -25   -20
114 GAC CGG CGG CTG CTG CTG CTT GTT GTT TTG TCA GTA ATG ATT CTT GAG      102
115 Asp Arg Arg Leu Leu Leu Leu Val Val Leu Ser Val Met Ile Leu Glu
116                               -15   -10   -5
118 ACC GTT ACA AAC CAA GAC CTG CCT GTG ATC AAG TGT GTT TTA ATC AGT      150
119 Thr Val Thr Asn Gln Asp Leu Pro Val Ile Lys Cys Val Leu Ile Ser
120                               1       5       10
122 CAT GAG AAC AAT GGC TCA TCA GCG GGA AAG CCA TCA TCG TAC CGA ATG      198
123 His Glu Asn Asn Gly Ser Ser Ala Gly Lys Pro Ser Ser Tyr Arg Met
124       15               20               25
126 GTG CGA GGA TCC CCA GAA GAC CTC CAG TGT ACC CCG AGG CGC CAG AGT      246
127 Val Arg Gly Ser Pro Glu Asp Leu Gln Cys Thr Pro Arg Arg Gln Ser
128       30               35               40               45
130 GAA GGG ACG GTA TAT GAA GCG GCC ACC GTG GAG GTG GCC GAG TCT GGG      294
131 Glu Gly Thr Val Tyr Glu Ala Ala Thr Val Glu Val Ala Glu Ser Gly
132               50               55               60
134 TCC ATC ACC CTG CAA GTG CAG CTC GCC ACC CCA GGG GAC CTT TCC TGC      342
135 Ser Ile Thr Leu Gln Val Gln Leu Ala Thr Pro Gly Asp Leu Ser Cys
136               65               70               75
138 CTC TGG GTC TTT AAG CAC AGC TCC CTG GGC TGC CAG CCG CAC TTT GAT      390
139 Leu Trp Val Phe Lys His Ser Ser Leu Gly Cys Gln Pro His Phe Asp
140               80               85               90
142 TTA CAA AAC AGA GGA ATC GTT TCC ATG GCC ATC TTG AAC GTG ACA GAG      438
143 Leu Gln Asn Arg Gly Ile Val Ser Met Ala Ile Leu Asn Val Thr Glu
144               95               100              105
146 ACC CAG GCA GGA GAA TAC CTA CTC CAT ATT CAG AGC GAA CGC GCC AAC      486

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147	Thr	Gln	Ala	Gly	Glu	Tyr	Leu	Leu	His	Ile	Gln	Ser	Glu	Arg	Ala	Asn	
148	110					115					120					125	
150	TAC	ACA	GTA	CTG	TTC	ACA	GTG	AAT	GTA	AGA	GAT	ACA	CAG	CTG	TAT	GTG	534
151	Tyr	Thr	Val	Leu	Phe	Thr	Val	Asn	Val	Arg	Asp	Thr	Gln	Leu	Tyr	Val	
152				130						135						140	
154	CTA	AGG	AGA	CCT	TAC	TTT	AGG	AAG	ATG	GAA	AAC	CAG	GAT	GCA	CTG	CTC	582
155	Leu	Arg	Arg	Pro	Tyr	Phe	Arg	Lys	Met	Glu	Asn	Gln	Asp	Ala	Leu	Leu	
156				145					150							155	
158	TGC	ATC	TCC	GAG	GGT	GTT	CCG	GAG	CCC	ACT	GTG	GAG	TGG	GTG	CTC	TGC	630
159	Cys	Ile	Ser	Glu	Gly	Val	Pro	Glu	Pro	Thr	Val	Glu	Trp	Val	Leu	Cys	
160			160						165							170	
162	AGC	TCC	CAC	AGG	GAA	AGC	TGT	AAA	GAA	GAA	GGC	CCT	GCT	GTT	GTC	AGA	678
163	Ser	Ser	His	Arg	Glu	Ser	Cys	Lys	Glu	Glu	Gly	Pro	Ala	Val	Val	Arg	
164		175						180								185	
166	AAG	GAG	GAA	AAG	GTA	CTT	CAT	GAG	TTG	TTC	GGA	ACA	GAC	ATC	AGA	TGC	726
167	Lys	Glu	Glu	Lys	Val	Leu	His	Glu	Leu	Phe	Gly	Thr	Asp	Ile	Arg	Cys	
168	190					195					200					205	
170	TGT	GCT	AGA	AAT	GCA	CTG	GGC	CGC	GAA	TGC	ACC	AAG	CTG	TTC	ACC	ATA	774
171	Cys	Ala	Arg	Asn	Ala	Leu	Gly	Arg	Glu	Cys	Thr	Lys	Leu	Phe	Thr	Ile	
172				210						215						220	
174	GAT	CTA	AAC	CAG	GCT	CCT	CAG	AGC	ACA	CTG	CCC	CAG	TTA	TTC	CTG	AAA	822
175	Asp	Leu	Asn	Gln	Ala	Pro	Gln	Ser	Thr	Leu	Pro	Gln	Leu	Phe	Leu	Lys	
176				225					230							235	
178	GTG	GGG	GAA	CCC	TTG	TGG	ATC	AGG	TGT	AAG	GCC	ATC	CAT	GTG	AAC	CAT	870
179	Val	Gly	Glu	Pro	Leu	Trp	Ile	Arg	Cys	Lys	Ala	Ile	His	Val	Asn	His	
180			240						245							250	
182	GGA	TTC	GGG	CTC	ACC	TGG	GAG	CTG	GAA	GAC	AAA	GCC	CTG	GAG	GAG	GGC	918
183	Gly	Phe	Gly	Leu	Thr	Trp	Glu	Leu	Glu	Asp	Lys	Ala	Leu	Glu	Glu	Gly	
184		255						260								265	
186	AGC	TAC	TTT	GAG	ATG	AGT	ACC	TAC	TCC	ACA	AAC	AGG	ACC	ATG	ATT	CGG	966
187	Ser	Tyr	Phe	Glu	Met	Ser	Thr	Tyr	Ser	Thr	Asn	Arg	Thr	Met	Ile	Arg	
188	270					275					280					285	
190	ATT	CTC	TTG	GCC	TTT	GTG	TCT	TCC	GTG	GGA	AGG	AAC	GAC	ACC	GGA	TAT	1014
191	Ile	Leu	Leu	Ala	Phe	Val	Ser	Ser	Val	Gly	Arg	Asn	Asp	Thr	Gly	Tyr	
192				290							295					300	
194	TAC	ACC	TGC	TCT	TCC	TCA	AAG	CAC	CCC	AGC	CAG	TCA	GCG	TTG	GTG	ACC	1062
195	Tyr	Thr	Cys	Ser	Ser	Ser	Lys	His	Pro	Ser	Gln	Ser	Ala	Leu	Val	Thr	
196				305						310						315	
198	ATC	CTA	GAA	AAA	GGG	TTT	ATA	AAC	GCT	ACC	AGC	TCG	CAA	GAA	GAG	TAT	1110
199	Ile	Leu	Glu	Lys	Gly	Phe	Ile	Asn	Ala	Thr	Ser	Ser	Gln	Glu	Glu	Tyr	
200			320						325							330	
202	GAA	ATT	GAC	CCG	TAC	GAA	AAG	TTC	TGC	TTC	TCA	GTC	AGG	TTT	AAA	GCG	1158
203	Glu	Ile	Asp	Pro	Tyr	Glu	Lys	Phe	Cys	Phe	Ser	Val	Arg	Phe	Lys	Ala	
204		335						340								345	
206	TAC	CCA	CGA	ATC	CGA	TGC	ACG	TGG	ATC	TTC	TCT	CAA	GCC	TCA	TTT	CCT	1206
207	Tyr	Pro	Arg	Ile	Arg	Cys	Thr	Trp	Ile	Phe	Ser	Gln	Ala	Ser	Phe	Pro	
208	350					355						360				365	
210	TGT	GAA	CAG	AGA	GGC	CTG	GAG	GAT	GGG	TAC	AGC	ATA	TCT	AAA	TTT	TGC	1254
211	Cys	Glu	Gln	Arg	Gly	Leu	Glu	Asp	Gly	Tyr	Ser	Ile	Ser	Lys	Phe	Cys	

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212				370				375				380					
214	GAT	CAT	AAG	AAC	AAG	CCA	GGA	GAG	TAC	ATA	TTC	TAT	GCA	GAA	AAT	GAT	1302
215	Asp	His	Lys	Asn	Lys	Pro	Gly	Glu	Tyr	Ile	Phe	Tyr	Ala	Glu	Asn	Asp	
216				385				390					395				
218	GAC	GCC	CAG	TTC	ACC	AAA	ATG	TTC	ACG	CTG	AAT	ATA	AGA	AAG	AAA	CCT	1350
219	Asp	Ala	Gln	Phe	Thr	Lys	Met	Phe	Thr	Leu	Asn	Ile	Arg	Lys	Lys	Pro	
220				400				405					410				
222	CAA	GTG	CTA	GCA	AAT	GCC	TCA	GCC	AGC	CAG	GCG	TCC	TGT	TCC	TCT	GAT	1398
223	Gln	Val	Leu	Ala	Asn	Ala	Ser	Ala	Ser	Gln	Ala	Ser	Cys	Ser	Ser	Asp	
224				415				420					425				
226	GGC	TAC	CCG	CTA	CCC	TCT	TGG	ACC	TGG	AAG	AAG	TGT	TCG	GAC	AAA	TCT	1446
227	Gly	Tyr	Pro	Leu	Pro	Ser	Trp	Thr	Trp	Lys	Lys	Cys	Ser	Asp	Lys	Ser	
228	430						435					440				445	
230	CCC	AAT	TGC	ACG	GAG	GAA	ATC	CCA	GAA	GGA	GTT	TGG	AAT	AAA	AAG	GCT	1494
231	Pro	Asn	Cys	Thr	Glu	Glu	Ile	Pro	Glu	Gly	Val	Trp	Asn	Lys	Lys	Ala	
232				450				455					460				
234	AAC	AGA	AAA	GTG	TTT	GGC	CAG	TGG	GTG	TCG	AGC	AGT	ACT	CTA	AAT	ATG	1542
235	Asn	Arg	Lys	Val	Phe	Gly	Gln	Trp	Val	Ser	Ser	Ser	Thr	Leu	Asn	Met	
236				465				470					475				
238	AGT	GAG	GCC	GGG	AAA	GGG	CTT	CTG	GTC	AAA	TGC	TGT	GCG	TAC	AAT	TCT	1590
239	Ser	Glu	Ala	Gly	Lys	Gly	Leu	Leu	Val	Lys	Cys	Cys	Ala	Tyr	Asn	Ser	
240				480				485					490				
242	ATG	GGC	ACG	TCT	TGC	GAA	ACC	ATC	TTT	TTA	AAC	TCA	CCA	GGC	CCC	TTC	1638
243	Met	Gly	Thr	Ser	Cys	Glu	Thr	Ile	Phe	Leu	Asn	Ser	Pro	Gly	Pro	Phe	
244				495				500					505				
246	CCT	TTC	ATC	CAA	GAC	AAC	ATC	TCC	TTC	TAT	GCG	ACC	ATT	GGG	CTC	TGT	1686
247	Pro	Phe	Ile	Gln	Asp	Asn	Ile	Ser	Phe	Tyr	Ala	Thr	Ile	Gly	Leu	Cys	
248	510					515					520				525		
250	CTC	CCC	TTC	ATT	GTT	GTT	CTC	ATT	GTG	TTG	ATC	TGC	CAC	AAA	TAC	AAA	1734
251	Leu	Pro	Phe	Ile	Val	Val	Leu	Ile	Val	Leu	Ile	Cys	His	Lys	Tyr	Lys	
252				530				535					540				
254	AAG	CAA	TTT	AGG	TAC	GAG	AGT	CAG	CTG	CAG	ATG	ATC	CAG	GTG	ACT	GGC	1782
255	Lys	Gln	Phe	Arg	Tyr	Glu	Ser	Gln	Leu	Gln	Met	Ile	Gln	Val	Thr	Gly	
256				545				550					555				
258	CCC	CTG	GAT	AAC	GAG	TAC	TTC	TAC	GTT	GAC	TTC	AGG	GAC	TAT	GAA	TAT	1830
259	Pro	Leu	Asp	Asn	Glu	Tyr	Phe	Tyr	Val	Asp	Phe	Arg	Asp	Tyr	Glu	Tyr	
260				560				565					570				
262	GAC	CTT	AAG	TGG	GAG	TTC	CCG	AGA	GAG	AAC	TTA	GAG	TTT	GGG	AAG	GTC	1878
263	Asp	Leu	Lys	Trp	Glu	Phe	Pro	Arg	Glu	Asn	Leu	Glu	Phe	Gly	Lys	Val	
264				575				580					585				
266	CTG	GGG	TCT	GGC	GCT	TTC	GGG	AGG	GTG	ATG	AAC	GCC	ACG	GCC	TAT	GGC	1926
267	Leu	Gly	Ser	Gly	Ala	Phe	Gly	Arg	Val	Met	Asn	Ala	Thr	Ala	Tyr	Gly	
268	590					595					600				605		
270	ATT	AGT	AAA	ACG	GGA	GTC	TCA	ATT	CAG	GTG	GCG	GTG	AAG	ATG	CTA	AAA	1974
271	Ile	Ser	Lys	Thr	Gly	Val	Ser	Ile	Gln	Val	Ala	Val	Lys	Met	Leu	Lys	
272				610				615					620				
274	GAG	AAA	GCT	GAC	AGC	TGT	GAA	AAA	GAA	GCT	CTC	ATG	TCG	GAG	CTC	AAA	2022
275	Glu	Lys	Ala	Asp	Ser	Cys	Glu	Lys	Glu	Ala	Leu	Met	Ser	Glu	Leu	Lys	
276				625				630					635				

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278	ATG	ATG	ACC	CAC	CTG	GGA	CAC	CAT	GAC	AAC	ATC	GTG	AAT	CTG	CTG	GGG	2070
279	Met	Met	Thr	His	Leu	Gly	His	His	Asp	Asn	Ile	Val	Asn	Leu	Leu	Gly	
280			640						645				650				
282	GCA	TGC	ACA	CTG	TCA	GGG	CCA	GTG	TAC	TTG	ATT	TTT	GAA	TAT	TGT	TGC	2118
283	Ala	Cys	Thr	Leu	Ser	Gly	Pro	Val	Tyr	Leu	Ile	Phe	Glu	Tyr	Cys	Cys	
284		655					660					665					
286	TAT	GGT	GAC	CTC	CTC	AAC	TAC	CTA	AGA	AGT	AAA	AGA	GAG	AAG	TTT	CAC	2166
287	Tyr	Gly	Asp	Leu	Leu	Asn	Tyr	Leu	Arg	Ser	Lys	Arg	Glu	Lys	Phe	His	
288	670					675					680					685	
290	AGG	ACA	TGG	ACA	GAG	ATT	TTT	AAG	GAA	CAT	AAT	TTC	AGT	TCT	TAC	CCT	2214
291	Arg	Thr	Trp	Thr	Glu	Ile	Phe	Lys	Glu	His	Asn	Phe	Ser	Ser	Tyr	Pro	
292					690				695						700		
294	ACT	TTC	CAG	GCA	CAT	TCA	AAT	TCC	AGC	ATG	CCT	GGT	TCA	CGA	GAA	GTT	2262
295	Thr	Phe	Gln	Ala	His	Ser	Asn	Ser	Ser	Met	Pro	Gly	Ser	Arg	Glu	Val	
296			705						710				715				
298	CAG	TTA	CAC	CCG	CCC	TTG	GAT	CAG	CTC	TCA	GGG	TTC	AAT	GGG	AAT	TCA	2310
299	Gln	Leu	His	Pro	Pro	Leu	Asp	Gln	Leu	Ser	Gly	Phe	Asn	Gly	Asn	Ser	
300			720						725				730				
302	ATT	CAT	TCT	GAA	GAT	GAG	ATT	GAA	TAT	GAA	AAC	CAG	AAG	AGG	CTG	GCA	2358
303	Ile	His	Ser	Glu	Asp	Glu	Ile	Glu	Tyr	Glu	Asn	Gln	Lys	Arg	Leu	Ala	
304		735					740					745					
306	GAA	GAA	GAG	GAG	GAA	GAT	TTG	AAC	GTG	CTG	ACG	TTT	GAA	GAC	CTC	CTT	2406
307	Glu	Glu	Glu	Glu	Glu	Asp	Leu	Asn	Val	Leu	Thr	Phe	Glu	Asp	Leu	Leu	
308	750					755					760					765	
310	TGC	TTT	GCG	TAC	CAA	GTG	GCC	AAA	GGC	ATG	GAA	TTC	CTG	GAG	TTC	AAG	2454
311	Cys	Phe	Ala	Tyr	Gln	Val	Ala	Lys	Gly	Met	Glu	Phe	Leu	Glu	Phe	Lys	
312				770					775						780		
314	TCG	TGT	GTC	CAC	AGA	GAC	CTG	GCA	GCC	AGG	AAT	GTG	TTG	GTC	ACC	CAC	2502
315	Ser	Cys	Val	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	Val	Leu	Val	Thr	His	
316			785						790					795			
318	GGG	AAG	GTG	GTG	AAG	ATC	TGT	GAC	TTT	GGA	CTG	GCC	CGA	GAC	ATC	CTG	2550
319	Gly	Lys	Val	Val	Lys	Ile	Cys	Asp	Phe	Gly	Leu	Ala	Arg	Asp	Ile	Leu	
320			800						805				810				
322	AGC	GAC	TCC	AGC	TAC	GTC	GTC	AGG	GGC	AAC	GCA	CGG	CTG	CCG	GTG	AAG	2598
323	Ser	Asp	Ser	Ser	Tyr	Val	Val	Arg	Gly	Asn	Ala	Arg	Leu	Pro	Val	Lys	
324		815						820				825					
326	TGG	ATG	GCA	CCC	GAG	AGC	TTA	TTT	GAA	GGG	ATC	TAC	ACA	ATC	AAG	AGT	2646
327	Trp	Met	Ala	Pro	Glu	Ser	Leu	Phe	Glu	Gly	Ile	Tyr	Thr	Ile	Lys	Ser	
328	830					835					840					845	
330	GAC	GTC	TGG	TCC	TAC	GGC	ATC	CTT	CTC	TGG	GAG	ATA	TTT	TCA	CTG	GGT	2694
331	Asp	Val	Trp	Ser	Tyr	Gly	Ile	Leu	Leu	Trp	Glu	Ile	Phe	Ser	Leu	Gly	
332					850					855					860		
334	GTG	AAC	CCT	TAC	CCT	GGC	ATT	CCT	GTC	GAC	GCT	AAC	TTC	TAT	AAA	CTG	2742
335	Val	Asn	Pro	Tyr	Pro	Gly	Ile	Pro	Val	Asp	Ala	Asn	Phe	Tyr	Lys	Leu	
336			865						870					875			
338	ATT	CAG	AGT	GGA	TTT	AAA	ATG	GAG	CAG	CCA	TTC	TAT	GCC	ACA	GAA	GGG	2790
339	Ile	Gln	Ser	Gly	Phe	Lys	Met	Glu	Gln	Pro	Phe	Tyr	Ala	Thr	Glu	Gly	
340			880						885				890				
342	ATA	TAC	TTT	GTA	ATG	CAA	TCC	TGC	TGG	GCT	TTT	GAC	TCA	AGG	AAG	CGG	2838

VERIFICATION SUMMARY

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L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]